

**IN THE SPECIFICATION:**

On page 5, please replace the paragraph starting on line 17 with the following:

Fig. 1 illustrates the amino acid sequence of EGIII from *Trichoderma longibrachiatum* (SEQ ID NO: 7).

On page 6, please replace the paragraph starting on line 1 with the following:

Fig. 6 illustrates an alignment of the full length sequence of 20 EGIII-like cellulases in alignment with EGIII, indicating equivalent residues based on primary sequence modeling, including those derived from *Trichoderma reesei* (SEQ ID NO: 8), *Hypocrea schweinitzii* (SEQ ID NO: 9), *Aspergillus aculeatus* (SEQ ID NO: 10), *Aspergillus kawachii* (1) (SEQ ID NO: 11), *Aspergillus kawachii* (2) (SEQ ID NO: 12), *Aspergillus oryzae* (SEQ ID NO: 13), *Humicola grisea* (SEQ ID NO: 14), *Humicola insolens* (SEQ ID NO: 15), *Chaetomium brasiliense* (SEQ ID NO: 16), *Fusarium equiseti* (SEQ ID NO: 17), *Fusarium javanicum* (1) (SEQ ID NO: 18), *Fusarium javanicum* (2) (SEQ ID NO: 19), *Gliocladium roseum* (1) (SEQ ID NO: 20), *Gliocladium roseum* (2) (SEQ ID NO: 21), *Gliocladium roseum* (3) (SEQ ID NO: 22), *Gliocladium roseum* (4) (SEQ ID NO: 23), *Memnoniella echinata* (SEQ ID NO: 24), *Emericella desertoru* (SEQ ID NO: 25), *Actinomyces 11AG8* (SEQ ID NO: 26), *Streptomyces lividans CelB* (SEQ ID NO: 27), *Rhodothermus marinus* (SEQ ID NO: 28), and *Erwinia carotovora* (SEQ ID NO: 29).